

PTO/PCT Rec'd 27 NOV 2000

APOPTOSIS MODULATORS THAT INTERACT WITH THE
HUNTINGTON'S DISEASE GENE

BACKGROUND OF THE INVENTION

This application relates to a family of apoptosis modulators that interact with the Huntington's Disease gene product, and to methods and compositions relating thereto.

"Interacting proteins" are proteins which associate *in vivo* to form specific complexes.

5 Non-covalent bonds, including hydrogen bonds, hydrophobic interactions and other molecular associations form between the proteins when two protein surfaces are matched or have affinity for each other. This affinity or match is required for the recognition of the two proteins, and the formation of an interaction. Protein-protein interactions are involved in the assembly of enzyme subunits; in antigen-antibody reactions; in forming the supramolecular
10 structures of ribosomes, filaments, and viruses; in transport; and in the interaction of receptors on a cell with growth factors and hormones.

Huntington's disease is an adult onset disorder characterized by selective neuronal loss in discrete regions of the brain and spinal chord that lead to progressive movement disorder, personality change and intellectual decline. From onset, which generally occurs around age
15 40, the disease progresses with worsening symptoms, ending in death approximately 18 years after onset.

The biochemical cause of Huntington's disease is unclear. While the biochemical cause of Huntington's disease has remained elusive, a mutation in a gene within chromosome 4p16.3 subband has been identified and linked to the disease. This gene, referred to as the
20 Huntington's Disease or HD gene, contains two repeat regions, a CAG repeat region and a CCG repeat region. Testing of Huntington's disease patients has shown that the CAG region is highly polymorphic, and that the number of CAG repeat units in the CAG repeat region is a very reliable indicator of having inherited the gene for Huntington's disease. Thus, in control individuals and in most individuals suffering from neuropsychiatric disorders other than
25 Huntington's disease, the number of CAG repeats is between 9 and 35, while in individuals suffering from Huntington's disease the number of CAG repeats is expanded and is 36 or greater.

To date, no differences have been observed at either the total RNA, mRNA or protein levels between normal and HD-affected individuals. Thus, the function of the HD protein and its role in the pathogenesis of Huntington's Disease remain to be elucidated.

5 SUMMARY OF THE INVENTION

We have now identified a protein designated as HIP1, that interact differently with the gene product of a normal (16 CAG repeat) and an expanded (>44 CAG repeat) HD gene. The HIP1 protein originally isolated from a yeast two-hybrid screen is encoded by a 1.2 kb cDNA (Seq. ID. No. 1), devoid of stop codons, that is expressed as a 400 amino acid
10 polypeptide (Seq. ID. No. 2). Subsequent study has elucidated additional sequence for HIP1 such that a 1090 amino acid protein is now known. (Seq. ID No. 5). Expression of the HIP1 protein was found to be enriched in the brain.

Analysis of the sequence of the HIP1 protein indicated that it includes a death effector domain (DED), suggesting an apoptotic function. Thus, it appears that a normal function of
15 huntingtin may be to bind HIP1 and related apoptosis modulators, reducing its effectiveness in stimulating cell death. Since expanded huntingtin performs this function less well, there is an increase in HIP1-modulated cell death in individuals with an expanded repeat in the HD gene. Furthermore, additional members of the same family of proteins have been identified which also contain a DED. Thus, the present invention provides a new class of apoptotic
20 modulators which are referred to as HIP-apoptosis modulating proteins.

This understanding of the likely role of huntingtin and HIP1 or related proteins in the pathology of Huntington's Disease offers several possibilities for therapy. First, because the function of huntingtin apparently depends at least in part on the ability to interact with HIP-apoptosis modulating proteins, added expression (e.g., via gene therapy) of normal (non-
25 expanded) huntingtin or of the HIP-binding region of huntingtin should provide a therapeutic benefit. Other DED-interacting peptides could also be used to mask and reduce the interaction of HIP-apoptosis modulating proteins with the death signaling complex. Alternatively, a mutant form of HIP-protein from which the DED has been deleted might be introduced, for example using gene therapy techniques. Because HIP-apoptosis modulating
30 proteins have been shown to self-associate, a protein with a deleted DED may compete with

endogenous HIP-protein in the formation of these associations, thereby reducing the amount of apoptotically-active HIP-protein.

BRIEF DESCRIPTION OF THE DRAWING

5 Fig. 1 graphically depicts the amount of interaction between HIP1 and Huntingtin proteins with varying lengths of polyglutamine repeat;

Fig. 2 compares the nucleic acid sequences of human and murine HIP1 and HIP1a;

Fig. 3 compares the amino acid sequences of human and murine HIP1 and HIP1a;

10 Fig. 4 shows the sequences of various death effector domains in comparison to the DED of human and murine HIP1 and HIP1a;

Fig. 5 shows the genomic organization of human HIP1;

Fig. 6 compares the sequences of human HIP1 with ZK370.3 protein of *C. elegans*;

Fig. 7 shows mouse EST's with homology to human HIP1 cDNA used to screen a mouse brain library;

15 Fig. 8 shows the affect of HIP1 on susceptibility of cells to stress; and

Figs. 9A - 9C show the toxicity of HIP1 in the presence of huntingtin with different lengths of polyglutamine repeats.

DETAILED DESCRIPTION OF THE INVENTION

20 This application relates to a new family of proteins function as modulators of apoptosis. At least some of these proteins, notably the human protein designated HIP1, interact with the gene product of the Huntington's disease gene. Other proteins within the family possess at least 40% and preferably more than 50% nucleotide identity with HIP1 and include a death effector domain (DED) . Such proteins are referred to in the specification and claims
25 hereof as "HIP-apoptosis modulating proteins."

The first HIP-apoptosis modulating protein identified was designated as HIP1. HIP1 was identified using the yeast two-hybrid system described in US Patent No. 5,283,173 which is incorporated herein by reference. Briefly, this system utilizes two chimeric genes or plasmids expressible in a yeast host. The yeast host is selected to contain a detectable marker
30 gene having a binding site for the DNA binding domain of a transcriptional activator. The

first chimeric gene or plasmid encodes a DNA-binding domain which recognizes the binding site of the selectable marker gene and a test protein or protein fragment. The second chimeric gene or plasmid encodes for a second test protein and a transcriptional activation domain. The two chimeric genes or plasmids are introduced into the host cell and expressed, and the cells are cultivated. Expression of the detectable marker gene only occurs when the gene product of the first chimeric gene or plasmid binds to the DNA binding domain of the detectable marker gene, and a transcriptional activation domain is brought into sufficient proximity to the DNA-binding domain, an occurrence which is facilitated by protein-protein interactions between the first and second test proteins. By selecting for cells expressing the detectable marker gene, those cells which contain chimeric genes or plasmids for interacting proteins can be identified, and the gene can be recovered and identified.

In testing for Huntington Interacting Proteins, several different plasmids were prepared containing portions of the human HD gene. The first four, identified as 16pGBT9, 44pGBT9, 80pGBT9 and 128pGBT9, were GAL4 DNA binding domain-HD in-frame fusions containing nucleotides 314 to 1955 (amino acids 1-540) of the published HD cDNA sequences cloned into the vector pGBT9 (Clontech). These plasmids contain a CAG repeat region of 16, 44, 80 and 128 glutamine-encoding repeats, respectively. A clone (DMK BamHIpGBT9) was made by fusing a cDNA encoding the first 544 amino acids of the myotonic dystrophy gene (a gift from R. Korneluk) in-frame with the GAL4-DNA BD of pGBT9 and was used as a negative control.

These plasmids have been used to identify and characterize HIP1, as well as two additional HD-interacting proteins, HIP2 and HIP3, which have not yet been tested for function as apoptosis modulators. These plasmids can be further used for the identification of additional interacting proteins which do act as apoptosis modulators, and for tests to refine the region on the protein in which the interaction occurs. Thus, one aspect of the invention is these four plasmids, and the use of these plasmids in identifying HD-interacting proteins. Furthermore, it will be appreciated that the GAL4 DNA-binding and activating domains are not the only domains which can be used in the yeast two-hybrid assay. Thus, in a broader sense, the invention encompasses any chimeric genes or plasmids containing nucleotides 314 to 1955 of the HD gene together with an activating or DNA-binding domain suitable for use

in the yeast one, two- or three-hybrid assay for proteins critical in either binding to the HD protein or responsible for regulated expression of the HD gene.

After introducing the plasmids into Y190 yeast host cells, transforming the host cells with an adult human brain Matchmaker™ (Clontech) cDNA library coupled with a GAL4 activating domain, and selecting for the expression of two detectable marker genes to identify clones containing genes for interacting proteins, the activating domain plasmids were recovered and analyzed. As a result of this analysis, three different cDNA fragments were identified as encoding for HD-interacting proteins and designated as HIP1, HIP2 and HIP3. The nucleic acid sequence of HIP1, as originally recovered in the yeast two-hybrid assay, is given in Seq. ID. No. 1. The polypeptide which it encodes is given by Seq. ID No. 2. Further investigation of the HIP1 cDNA resulted in the characterization of a longer region of cDNA totaling 4795 bases and a corresponding protein, the sequences of which are given by Seq ID Nos. 3 and 4, respectively. A further portion of the HIP1 protein was characterized, extending the length to the complete protein sequence of 1090 amino acids (Seq. ID No. 5)

The cDNA molecules encoding HIP-apoptosis modulating proteins, particularly those encoding portions of HIP1, can be explored using oligonucleotide probes for example for amplification and sequencing. In addition, oligonucleotide probes complementary to the cDNA can be used as diagnostic probes to localize and quantify the presence of HIP1 DNA. Probes of this type with a one or two base mismatch can also be used in site-directed mutagenesis to introduce variations into the HIP1 sequence which may increase or decrease the apoptotic activity. Preferred targets for such mutations would be the death effector domains. Thus, a further aspect of the present invention is an oligonucleotide probe, preferably having a length of from 15-40 bases which specifically and selectively hybridizes with the cDNA given by Seq. ID No. 1 or 3 or a sequence complementary thereto. As used herein, the phrase "specifically and selectively hybridizes with" the cDNA refers to primers which will hybridize with the cDNA under stringent hybridization conditions.

Probes of this type can also be used for diagnostic purposes to characterize risk of Huntington's Disease like symptoms arising in individuals where the symptoms are present in the family history but are not associated with an expansion of the CAG repeat. Such symptoms may arise from a mutation in HIP1 or other HIP-apoptosis modulating protein

which alters the interaction of this protein with huntingtin, thereby increasing the apoptotic activity of the protein even in the presence of a normal (non-expanded) huntingtin molecule. An appropriate probe for this purpose would one which hybridizes with or adjacent to the huntingtin binding region of the HIP-apoptosis modulating protein. In HIP1, this lies within amino acids 129-514.

DNA sequencing of the HIP1 cDNA initially isolated from the yeast two-hybrid screen (Seq. ID No. 1) revealed a 1.2 kb cDNA that shows no significant degree of nucleic acid identity with any stretch of DNA using the blastn program at ncbi (blast@ncbi.nlm.nih.gov). When the larger HIP1 cDNA sequence (SEQ ID NO. 3) was translated into a polypeptide, the HIP1 cDNA coding (nucleotides 328-3069) is observed to be devoid of stop codons, and to produce a 914 amino acid polypeptide. A polypeptide identity search revealed an identity match over the entire length of the protein (46% conservation) with that of a hypothetical protein from *C. elegans* (ZK370.3 protein; *C. elegans* cosmid ZK370). This *C. elegans* protein shares identity with the mouse talin gene, which encodes a 217 kDa protein implicated with maintaining integrity of the cytoskeleton. It also shares identity with the SLA2/MOP2/ END4 gene from *Saccharomyces cerevisiae*, which is known to code for an essential cytoskeletal associated gene required for the accumulation and or maintenance of plasma membrane H⁺-ATPase on the cell surface. When pairwise comparisons are performed between HIP1 and the *C. elegans* ZK370.3 protein (Genpept accession number celzk370.3), it shows 26% complete identity and an overall 46% level of conservation. Comparative analysis between HIP1 and SLA2/MOP2/ END4 (EMBL accession number Z22811) demonstrate similar conservation (20% identity, 40% conservation).

Further exploration revealed several important facts about HIP1 that implicate it in a significantly in the pathogenesis of Huntington's Disease. First, as shown in Fig. 1, it was found that the native interaction between HD protein and HIP1 is influenced by the number of CAG repeats. Second, it was found that expression of the HIP1 protein is enriched in the brain. The highest amounts of expression are in the cortex, with lower levels being seen in the cerebellum, caudate and putamen.

It has also been observed that huntingtin proteins with expanded polyglutamine tracts can aggregate into large, irregularly shaped deposits in HD brains, transgenic mice and *in vitro* cell culture. We have shown that in HEK (human embryonic kidney) 293T cells, the aggregation of full-length and smaller huntingtin fragments occurs after the cells have been exposed to a period of apoptotic stress. Martindale, et al., *Nature Genetics* 18: 150-154 (1998). In order to assess the consequence of HIP1 expression in cultured cells, we used huntingtin aggregation as one marker of viability. What we found was that cells cotransfected with huntingtin (128 CAG repeats) and HIP1 contained aggregates comparable to those observed following application of apoptotic stress with sub-lethal doses of tamoxifen in 14% of the cells, and that these cells were the ones in which both genes had been introduced as reflected by a double marker experiment. Transfection of a gene encoding a fusion protein of 128 repeat huntingtin and the DED domain from HIP1 ligated in the sense orientation resulted in aggregate formation in 30 to 50% of the cells.

The implications of the apoptotic activity of HIP1 are two-fold. First, the fact that this activity is apparently differentially modulated by interaction with huntingtin having normal and expanded repeats implicates HIP1 in the apoptotic neuronal death which is observed in Huntington's disease and makes HIP1 a logical target for therapy. A second implication of the apoptotic activity of HIP1 is the potential for use of HIP1 as a therapeutic agent to introduce apoptosis in cancer cells.

Therapeutic targeting of HIP1 or other HIP-apoptosis modulating proteins might take any of several forms, but will in general be a treatment involving administration of a composition that reduces the apoptotic activity of the HIP-apoptosis modulating protein. As used in the specification and claims hereof, the term "administration" includes direct administration of a composition active to reduce apoptotic activity as well as indirect administration which might include administration of pro-drugs or nucleic acids that encode the desired therapeutic composition.

One class of composition which can be used in the therapeutic methods of the invention are those compositions which interfere with the activity of HIP-apoptosis modulating proteins by binding to the proteins and mask and reduce the interaction of HIP-apoptosis modulating proteins with the death signaling complex. Within this class of

compositions are normal (non-expanded) huntingtin, administered, for example, via increased expression of exogenous HD genes; the HIP-binding region of huntingtin, administered via gene therapy techniques; and other DED-interacting peptides. Other DED-interacting peptides which might be used in a therapeutic method of this type include FADD (Beldin et al., *Cell* 85: 803-815 (1996)) and caspase 8 (Muzio et al., *Cell* 85: 817-827 (1996)).

An alternative form of therapy involves the use of a mutant form of HIP1 or other HIP-apoptosis modulating protein from which the DED has been deleted. DED-containing proteins, including HIP1 are self-associating, and this self-association has been shown to be important for activity. (Muzio et al., *Cell* 85: 817-827 (1996)). Thus, a protein with a deleted DED may compete with endogenous HIP-protein in the formation of these associations, thereby reducing the amount of apoptotically-active HIP-protein.

In addition to HIP1, we have identified a further human protein, HIP1a, from a human frontal cortex cDNA library. HIP1a is a family member of HIP1, and thus a HIP-apoptosis modulator in accordance with the invention. A partial sequence of HIP1a (the 5' portion of HIP1a remains to be characterized) is given by SEQ ID Nos. 6 and 7. The isolated and characterized portion of HIP1a shows 53% nucleotide identity and 58% amino acid conservation with HIP1 (Table 1, Figs. 2 and 3).

We have also isolated 2 mouse proteins mHIP1 and mHIP1a (SEQ. ID Nos. 8-11) which appear to be the murine homologues of human HIP1 and HIP1a. As in the case of human HIP1a, the 5' portion of mHIP1 remains to be isolated. At present, mHIP1 shows 85% nucleotide identity and 90% amino acid conservation with huHIP1 (Table 1, Figs. 2 and 3). mHIP1a shows 60% nucleotide identity and 61% amino acid conservation with huHIP1 (Table 1, Figs. 2 and 3). mHIP1a shows stronger homology to huHIP1a; it shows 87% nucleotide identity and 91% amino acid conservation with huHIP1a (Table 1, Figs. 2 and 3). Taken together these findings indicate that mHIP1 is the murine homologue of huHIP1 whereas mHIP1a is most likely the murine homologue of huHIP1a. As mentioned previously, HIP1 shows sequence similarity to Sla2p in *S. cerevisiae* and the hypothetical protein ZK370.3 in *C. elegans*. Similarly, huHIP1a, mHIP1, and mHIP1a show sequence similar to Sla2p and ZK370.3 (Table 2). The carboxy-terminal regions of huHIP1a, mHIP1, and mHIP1a all show considerable homology to the mammalian membrane

cytoskeletal-associated protein, talin. This suggests that these 3 proteins may also play a role in the regulation of membrane events through interactions with the underlying cytoskeleton.

HIP1 contains a death effector domain (DED), a domain which is also present in a number of proteins involved in the apoptotic pathway (Fig. 4). This suggests that HIP1 may act as a modulator of the apoptosis pathway. The DED in huHIP1 is present between amino acid positions 287 and 368. Similarly, HIP1a, mHIP1, and mHIP1a also contain a DED. In huHIP1a the DED is present at amino acids 1-78 of the recovered fragment. In mHIP1 and mHIP1a, the DED are present at amino acids 128- 210 and 388-470, respectively. The DED present in huHIP1a, mHIP1 and mHIP1a all show significant percentage amino acid conservation to the DED present in huHIP1 (Table 3).

Increasing expression of normal (non-expanded) huntingtin or the HIP-apoptotic modulator-binding portion thereof, a modified HIP-apoptotic modulator in which the DED has been deleted or of a DED-interacting protein or peptide can be accomplished using gene therapy approaches. In general, this will involve introduction of DNA encoding the appropriate protein or peptide in an expressable vector into the brain cells. Expression of HIP-apoptosis modulating proteins may also be useful in treatment of cancer in which case application to other cell types would be desired, and cells expressing HIP-apoptosis modulating proteins may be used for screening of therapeutic compounds. Thus, in a more general sense, expression vectors are defined herein as DNA sequences that are required for the transcription of cloned copies of genes and the translation of their mRNAs in an appropriate cell type. Specifically designed vectors allow the shuttling of DNA between hosts such as bacteria-yeast or bacteria-animal cells. An appropriately constructed expression vector may contain: an origin of replication for autonomous replication in host cells, selectable markers, a limited number of useful restriction enzyme sites, a potential for high copy number, and active promoters. A promoter is defined as a DNA sequence that directs RNA polymerase to bind to DNA and initiate RNA synthesis. A strong promoter is one which causes mRNAs to be initiated at high frequency. Expression vectors may include, but are not limited to, cloning vectors, modified cloning vectors, specifically designed plasmids or viruses.

A variety of mammalian expression vectors may be used to express recombinant

HIP-apoptosis modulating proteins or fragments thereof in mammalian cells. Commercially available mammalian expression vectors which may be suitable for recombinant HIP-apoptosis modulating protein expression, include but are not limited to, pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593) 5 pBPV-1(8-2) (ATCC 37110), pdBPV-MMTneo(342-12) (ATCC 37224), pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCtag (ATCC 37460), and IZD35 (ATCC 37565). Other vectors which have been shown to be suitable expression systems in mammalian cells include the herpes simplex viral based vectors: pHSV1 (Geller et al. Proc. Natl. Acad. Sci. 87:8950-8954 (1990)); recombinant retroviral vectors: MFG 10 (Jaffee et al. Cancer Res. 53:2221-2226 (1993)); Moloney-based retroviral vectors: LN, LNSX, LNCX, LXSX (Miller and Rosman Biotechniques 7:980-989 (1989)); vaccinia viral vector: MVA (Sutter and Moss Proc. Natl. Acad. Sci. 89:10847-10851 (1992)); recombinant adenovirus vectors : pJM17 (Ali et al Gene Therapy 1:367-384 (1994)), (Berkner K. L. Biotechniques 6:616-624 1988); second generation adenovirus vector: DE1/DE4 adenoviral 15 vectors (Wang and Finer Nature Medicine 2:714-716 (1996)); and Adeno-associated viral vectors: AAV/Neo (Muro-Cacho et al. J. Immunotherapy 11:231-237 (1992)).

The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transformation, transfection, infection, protoplast fusion, and electroporation. The expression vector-containing cells are clonally propagated 20 and individually analyzed to determine whether they produce the desired protein. Delivery of retroviral vectors to brain and nervous system tissue has been described in US Patents Nos. 4,866,042, 5,082,670 and 5,529,774, which are incorporated herein by references. These patents disclose the use of cerebral grafts or implants as one mechanism for introducing vectors bearing therapeutic gene sequences into the brain, as well as an approach in which the 25 vectors are transmitted across the blood brain barrier.

To further illustrate the methods of making the materials which are the subject of this invention, and the testing which has established their utility, the following non-limiting experimental procedures are provided.

EXAMPLE 1

IDENTIFICATION OF INTERACTING PROTEINS

GAL4-HD cDNA constructs

An HD cDNA construct (44pGBT9), with 44 CAG repeats was generated encompassing amino acids 1 - 540 of the published HD cDNA . This cDNA fragment was fused in frame to the GAL4 DNA-binding domain (BD) of the yeast two-hybrid vector pGBT9 (Clontech). Other HD cDNA constructs, 16pGBT9, 80pGBT9 and 128pGBT9 were constructed, identical to 44pGBT9 but included only 16, 80 or 128 CAG repeats, respectively.

Another clone (DMKDBamHIpGBT9) containing the first 544 amino acids of the myotonic dystrophy gene (a gift from R. Korneluk) was fused in-frame with the GAL4-DNA BD of pGBT9 and was used as a negative control. Plasmids expressing the GAL4-BDRAD7 (D. Gietz, unpublished) and SIR3 were used as a positive control for the β -galactosidase filter assay.

The clones IT15-23Q, IT15-44Q and HAP1 were generous gifts from Dr. C. Ross. These clones represent a previously isolated huntingtin interacting protein that has a higher affinity for the expanded form of the HD protein.

Yeast strains, transformations and β -galactosidase assays

The yeast strain Y190 (MATa leu2-3,112, ura3-52, trp1-901, his3- Δ 200, ade2-101, gal4 Δ gal80 Δ , URA3::GAL-lacZ, LYS2::GAL-HIS3,cyc^r) was used for all transformations and assays. Yeast transformations were performed using a modified lithium acetate transformation protocol and grown at 30 C using appropriate synthetic complete (SC) dropout media.

The β -galactosidase chromogenic filter assays were performed by transferring the yeast colonies onto Whatman filters. The yeast cells were lysed by submerging the filters in liquid nitrogen for 15-20 seconds. Filters were allowed to dry at room temperature for at least five minutes and placed onto filter paper presoaked in Z-buffer (100 mM sodium phosphate (pH7.0) 10 mM KCl, 1 mM MgSO₄) supplemented with 50 mM

2-mercaptoethanol and 0.07 mg/ml 5-bromo-4-chloro-3-indolyl β -D-galactoside (X-gal). Filters were placed at 37 C for up to 8 hours.

Yeast two-hybrid screening for huntingtin interacting protein (HIP)

5 cDNAs from an human adult brain Matchmaker™ cDNA library (Clontech) was transformed into the yeast strain Y190 already harboring the 44pGBT9 construct. The transformants were plated onto one hundred 150 mm x 15 mm circular culture dishes containing SC media deficient in Trp, Leu and His. The herbicide 3-amino-triazole (3-AT) (25mM) was utilized to limit the number of false His⁺ positives (31). The yeast
10 transformants were placed at 30 C for 5 days and β -galactosidase filter assays were performed on all colonies found after this time, as described above, to identify β -galactosidase⁺ clones. Primary His⁺/ β -galactosidase⁺ clones were then orderly patched onto a grid on SC -Trp/-Leu/-His (25 mM 3AT) plates and assayed again for His⁺ growth and the ability to turn blue with a filter assay. Secondary positives were identified for further analysis. Proteins
15 encoded by positive cDNAs were designated as HIPs (Huntingtin Interactive Proteins). Approximately 4.0×10^7 Trp/Leu auxotrophic transformants were screened and of 14 clones isolated 12 represented the same cDNA (HIP1), and the other 2 cDNAs, HIP2 and HIP3 were each represented only once.

The HIP cDNA plasmids were isolated by growing the His⁺/ β -galactosidase⁺ colony
20 in SC -Leu media overnight, lysing the cells with acid-washed glass beads and electroporating the bacterial strain, KC8 (leuB auxotrophic) with the yeast lysate. The KC8 ampicillin resistant colonies were replica plated onto M9 (-Leu) plates. The plasmid DNA from M9⁺ colonies was transformed into DH5-a for further manipulation.

EXAMPLE 2

CONFIRMATION OF INTERACTIONS

25 The HIP1-GAL4-AD cDNA activated both the lac-Z and His reporter genes in the yeast strain Y190 only when co-transformed with the GAL4-BD-HD construct, but not the negative controls (Fig. 1) of the vector alone or a random fusion protein of the myotonin
30 kinase gene. In order to assess the influence of the polyglutamine tract on the interaction

between HIP1 and HD, semi-quantitative β -galactosidase assays were performed.

GAL4-BD-HD fusion proteins with 16, 44, 80 and 128 glutamine repeats were assayed for their strength of interaction with the GAL4-AD-HIP1 fusion protein.

Liquid β -galactosidase assays were performed by inoculating a single yeast colony into appropriate synthetic complete (SC) dropout media and grown to OD600 0.6-1.5. Five millilitres of overnight culture was pelleted and washed once with 1 ml of Z-Buffer, then resuspended in 100 ml Z-Buffer supplemented with 38 mM 2-mercaptoethanol, and 0.05% SDS. Acid washed glass beads (~100 ml) were added to each sample and vortexed for four minutes, by repeatedly alternating a 30 seconds vortex, with 30 seconds on ice. Each sample was pelleted and 10 ml of lysate was added to 500 ml of lysis buffer. The samples were incubated in a 30 C waterbath for 30 seconds and then 100 ml of a 4 mg/ml o-nitrophenyl b-D galactopyranoside (ONPG) solution was added to each tube. The reaction was allowed to continue for 20 minutes at 30 C and stopped by the addition of 500 ml of 1 M Na₂CO₃ and placing the samples on ice. Subsequently, OD420 was taken in order to calculate the β -galactosidase activity with the equation $1000 \times OD420 / (t \times V \times OD600)$ where t is the elapsed time (minutes) and V is the amount of lysate used.

The specificity of the HIP1-HD interaction can be observed using the chromogenic filter assay. Only yeast cells harboring HIP1 and HD activate both the HIS and lacZ reporter genes in the Y190 yeast host. The cells that contain the HIP1 with HD constructs with 80 or 128 CAG repeats turn blue approximately 45 minutes after the cells with the smaller sized repeats (16 or 44).

No difference in the β -galactosidase activity was observed between the 16 and 44 repeats or between the 80 and 128 repeats. However, a significant difference ($p < 0.05$) in activity is seen between the smaller repeats (16 and 44) and the larger repeats (80 and 128). (Figure 1)

EXAMPLE 3

DNA SEQUENCING, cDNA ISOLATION AND 5' RACE

Oligonucleotide primers were synthesized on an ABI PCR-mate oligo-synthesizer.

DNA sequencing was performed using an ABI 373 fluorescent automated DNA sequencer.

The HIP cDNAs were confirmed to be in-frame with the GAL4-AD by sequencing across the AD-HIP1 cloning junction using an AD oligonucleotide (5'GAA GAT ACC CCA CCA AAC3'). (Seq. ID No. 12)

Subsequently, primer walking was used to determine the remaining sequences. A human frontal cortex >4.0 kb cDNA library (a gift from S. Montal) was screened to isolate the full length HIP1 gene. Fifty nanograms of a 558 base pair Eco RI fragment from the original HIP1 cDNA was radioactively labeled with [α^{32} P]-dCTP using nick-translation and the probe allowed to hybridized to filters containing >105 pfu/ml of the cDNA library overnight at 65 °C in Church buffer (see Northern blot protocol). The filters were washed at 65 °C for 10 minutes with 1 X SSPE, 15 minutes at 65 C with 1 X SSPE and 0.1% SDS, then for thirty minutes and fifteen minutes with 1 X SSPE and 0.1% SDS. The filters were exposed to X-ray film (Kodak, XAR5) overnight at -70 C. Primary positives were isolated and replated and subsequent secondary positives were hybridized and washed as for the primary screen. The resulting positive phage were converted into plasmid DNA by conventional methods (Stratagene) and the cDNA isolated and sequenced.

In order to obtain the most 5' sequence of the HIP1 gene, a Rapid Amplification of cDNA Ends (RACE) protocol was performed according to the manufacturers recommendations (BRL). First strand cDNA was synthesized using the oligo HIP1-242R (5' GCT TGA CAG TGT AGT CAT AAA GGT GGC TGC AGT CC 3'). (Seq. ID No. 13) After dCTP tailing the cDNA with terminal deoxy transferase, two rounds of 35 cycles (94 °C 1 minute; 53 °C 1 minute; 72 °C 2 minutes) of PCR using HIP1-R2 (5' GGA CAT GTC CAG GGA GTT GAA TAC 3') (Seq. ID No. 14) and an anchor primer (5' (CUA)4 GGC CAC GCG TCG ACT AGT ACG GGI IGG GII GGG IIG3') (BRL ,Seq. ID No. 15)) were performed. The subsequent 650 base pair PCR product was cloned using the TA cloning system (Invitrogen) and sequenced using T3 and T7 primers. Sequences ID Nos. 1 and 3 show the sequence of the HIP1 cDNAs obtained.

EXAMPLE 4

DNA AND AMINO ACID ANALYSES

Overlapping DNA sequence was assembled using the program MacVector and sent via email or Netscape to the BLAST server at NIH (<http://www.ncbi.nlm.nih.gov>) to search for sequence similarities with known DNA (blastn) or protein (tblastn) sequences. Amino acid alignments were performed with the program Clustalw.

EXAMPLE 5

FISH DETECTION SYSTEM AND IMAGE ANALYSIS

The HIP1 cDNA isolated from the two-hybrid screen was mapped by fluorescent in situ hybridization (FISH) to normal human lymphocyte chromosomes counterstained with propidium iodide and DAPI. Biotinylated probe was detected with avidin-fluorescein isothiocyanate (FITC). Images of metaphase preparations were captured by a thermoelectrically cooled charge coupled camera (Photometrics). Separate images of DAPI banded chromosomes and FITC targeted chromosomes were obtained. Hybridization signals were acquired and merged using image analysis software and pseudo colored blue (DAPI) and yellow (FITC) as described and overlaid electronically. This study showed that HIP1 maps to a single genomic locus at 7q11.2.

EXAMPLE 6

NORTHERN BLOT ANALYSIS

RNA was isolated using the single step method of homogenization in guanidinium isothiocyanate and fractionated on a 1.0% agarose gel containing 0.6 M formaldehyde. The RNA was transferred to a hybond N -membrane (Amersham) and crosslinked with ultraviolet radiation.

Hybridization of the Northern blot with b-actin as an internal control probe provided confirmation that the RNA was intact and had transferred. The 1.2 kb HIP1 cDNA was labeled using nick translation and incorporation of $\alpha^{32}\text{P}$ -dCTP. Hybridization of the original 1.2 kb HIP1 cDNA was carried out in Church buffer (0.5 M sodium phosphate buffer, pH 7.2, 2.7% sodium dodecyl sulphate, 1 mM EDTA) at 55 C overnight. Following

hybridization, Northern blots were washed once for 10 minutes in 2.0 X SSPE, 0.1% SDS at room temperature and twice for 10 minutes in 0.15 X SSPE, 0.1% SDS. Autoradiography was carried out from one to three days using Hyperfilm (Amersham) film at -70 C.

Analysis of the levels of RNA levels of HIP1 by Northern blot data revealed that the 10 kilo base HIP1 message is present in all tissue assessed. However, the levels of RNA are not uniform, with brain having highest levels of expression and peripheral tissues having less message. No apparent differences in RNA expression was noted between control samples and HD affected individuals.

EXAMPLE 7

TISSUE LOCALIZATION OF HIP1

Tissue localization of HIP1 was studied using a variety of techniques as described below. Subcellular distribution of HIP-1 protein in adult human and mouse brain Biochemical fractionation studies revealed the HIP1 protein was found to be a membrane-associated protein. No immunoreactivity was seen by Western blotting in cytosolic fractions, using the anti-HIP1-pep1 polyclonal antibody. HIP1 immunoreactivity was observed in all membrane fractions including nuclei (P1), mitochondria and synaptosomes (P2), microsomes and plasma membranes (P3). The P3 fraction contained the most HIP1 compared to other membrane fractions. HIP1 could be removed from membranes by high salt (0.5M NaCl) buffers indicating it is not an integral membrane protein, however, since low salt (0.1- 0.25M NaCl) was only able to partially remove HIP1 from membranes, its membrane association is relatively strong. The extraction of P3 membranes with the non-ionic detergent, Triton X-100 revealed HIP1 to be a Triton X-100 insoluble protein. This characteristic is shared by many cytoskeletal and cytoskeletal-associated membrane proteins including actin, which was used as a control in this study. The biochemical characteristics of HIP1 described were found to be identical in mouse and human brain and was the same for both forms of the protein (both bands of the HIP1 doublet). HIP1 co-localized with huntingtin in the P2 and P3 membrane fractions, including the high-salt membrane extractions, as well as in the Triton X-100 insoluble residue. The subcellular distribution of HIP1 was unaffected by the

expression of polyglutamine-expanded huntingtin in transgenic mice and HD patient brain samples.

The localization of HIP1 protein was further investigated by immunohistochemistry in normal adult mouse brain tissue. Immunoreactivity was seen in a patchy, reticular pattern in the cytoplasm, appeared excluded from the nucleus and stained most intensely in a discontinuous pattern at the membrane. These results are consistent with the association of HIP1 with the cytoskeletal matrix and further indicate an enrichment of HIP1 at plasma membranes. Immunoreactivity occurred in all regions of the brain, including cortex, striatum, cerebellum and brainstem, but appeared most strongly in neurons and especially in cortical neurons. As described previously, huntingtin immunoreactivity was seen exclusively and uniformly in the cytosol.

The in situ hybridization studies showed HIP1 mRNA to be ubiquitously and generally expressed throughout the brain. This data is consistent with the immunohistochemical results and was identical to the distribution pattern of huntingtin mRNA in transgenic mouse brains expressing full-length human huntingtin.

Protein Preparation And Western Blotting For Expression Studies

Frozen human tissues were homogenized using a Polytron in a buffer containing 0.25M sucrose, 20mM Tris-HCl (pH 7.5), 10mM EGTA, 2mM EDTA supplemented with 10ug/ml of leupeptin, soybean trypsin inhibitor and 1mM PMSF, then centrifuged at 4,000rpm for 10' at 4 C to remove cellular debris. 100-150ug/lane of protein was separated on 8% SDS-PAGE mini-gels and then transferred to PVDF membranes. Huntingtin and HIP1 were electroblotted overnight in Towbin's transfer buffer (25 mM Tris-HCl, 0.192M glycine, pH8.3, 10% methanol) at 30V onto PVDF membranes (Immobilon-P, Millipore) as described (Towbin et al, *Proc. Nat'l Acad. Sci.(USA)* 76: 4350-4354 (1979)). Membranes were blocked for 1 hour at room temperature in 5% skim milk/ TBS (10mM Tris-HCl, 0.15M NaCl, pH7.5). Antibodies against huntingtin (pAb BKP1, 1:500), actin (mAb A-4700, Sigma, 1:500) or HIP1 (pAb HIP-pep1, 1:200) were added to blocking solution for 1 hour at room temperature. After 3 x 10 minutes washes in TBS-T (0.05% Tween-20/TBS), secondary Ab (horseradish peroxidase conjugated IgG, Biorad) was applied in blocking solution for 1 hour

at room temperature. Membranes were washed and then incubated in chemiluminescent ECL solution and visualized using Hyperfilm-ECL film (Amersham).

Generation of Antibodies

5 The generation of huntingtin specific antibodies GHM1 and BKP1 is described elsewhere (Kalchman, et al., *J. Biol. Chem.* 271: 19385-19394 (1996)). The HIP1 peptide (VLEKDDLMDMDASQQN, a.a. 76-91 of Seq. ID No. 2) was synthesized with Cys on the N-terminus for the coupling, and coupled to Keyhole limpet hemocyanin (KLH) (Pierce) with succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (Pierce). Female
10 New Zealand White rabbits were injected with HIP1 peptide-KLH and Freund's adjuvant. Antibodies against the HIP1 peptide were purified from rabbit sera using affinity column with low pH elution. Affinity column was made by incubation of HIP1 peptide with activated thio-Sepharose (Pharmacia).

15 Western blotting of various peripheral and brain tissues were consistent with the RNA data. The HIP1 protein levels observed was not equivalent in all tissues. The protein expression is predominant in brain tissue, with highest amounts seen in the cortex and lower levels seen in the cerebellum and caudate and putamen.

20 More regio-specific analysis of HIP1 expression in the brain revealed no differential expression pattern in affected individuals when compared to normal controls, with highest levels of expression seen in both controls and HD patients in the cortical regions.

EXAMPLE 8

CO-IMMUNOPRECIPITATION OF HIP1 WITH HUNTINGTIN

25 Confirmation of the HD-HIP1 interaction was performed using coimmunoprecipitation as follows. Control human brain (frontal cortex) lysate was prepared in the same manner as for subcellular localization study. Prior to immunoprecipitation, tissue lysate was centrifuged at 5000 rpm for 2 minutes at 4°C, then the supernatant was pre-cleared by the incubated with excess amount of Protein A-Sepharose for 30 minutes at 4°C, and centrifuged at the same condition. Fifty microlitres of supernatant (500 mg protein) was incubated with or without antibodies (10 ug of anti-huntingtin GHM1 (Kalchman, et al. 1996)
30 or anti-synaptobrevin antibody) in the total 500 ul of incubation buffer (20mM Tris-Cl

(pH7.5), 40mM NaCl, 1mM MgCl₂) for 1 hour at 4°C. Twenty microlitres of Protein A-Sepharose (1:1 suspension, for GHM1 and no antibody control) or Protein G-Sepharose (for anti-synaptobrevin antibody; Pharmacia) was added and incubated for 1 hour at 4°C. The beads were washed with washing buffer (incubation buffer containing 0.5 % Triton X-100) three times. The samples on the beads were separated using SDS-PAGE (7.5% acrylamide) and transferred to PVDF membrane (Immobilon-P, Millipore). The membrane was cut at about 150 kDa after transfer for Western blotting (as described above). The upper piece was probed with anti-huntingtin BKP1 (1/1000) and lower piece with anti-HIP1 antibody (1/300).

The results showed that when an anti-HIP1 polyclonal antibody was immunoreacted against a blot containing the GHM1 immunoprecipitates from the brain lysate a doublet was observed at approximately 100 kDa. When GHM1 was immunoreacted against the same immunoprecipitate the 350 kDa HD protein was also seen. The specificity of the HD-HIP1 interaction is seen as no immunoreactive bands seen are as a result of the proteins adsorbing to the Protein-A-Sepharose (Lysate + No Antibody) or when a random, non related antibody (Lysate + anti-Synaptobrevin) is used as the immunoprecipitating antibody.

EXAMPLE 9

Subcellular fractionation of brain tissue

Cortical tissue (20-100 mg/ml) was homogenized, on ice, in a 2 ml pyrex-teflon IKA-RW15 homogenizer (Tekmar Company) in a buffer containing 0.303M sucrose, 20mM Tris-HCl pH 6.9, 1mM MgCl₂, 0.5mM EDTA, 1mM PMSF, 1mM leupeptin, soybean trypsin inhibitor and 1mM benzamidine (Wood et al., *Human Molec. Genet.* 5: 481-487 (1996)).

Crude membrane vesicles were isolated by two cycles of a three-step differential centrifugation protocol in a Beckman TLA 120.2 rotor at 4°C based on the methods of Wood et al (1996). The first step precipitated cellular debris and nuclei from tissue homogenates for 5 minutes at 1300 x g (P1). The 1300 x g supernatant was subsequently centrifuged for 20 minutes at 14 000 x g to isolate synaptosomes and mitochondria (P2). Finally, microsomal

and plasma membrane vesicles were collected by a 35 minute centrifugation at 142 000 x g (P3). The remaining supernatant was defined as the cytosolic fraction.

High salt extraction of membranes

- 5 Aliquots of P3 membranes were twice suspended at 2mg/ ml in 0.5M NaCl, 10mM Tris-HCl, 2mM MgCl₂, pH7.2, containing protease inhibitors (see above). The same buffer without NaCl was used as a control. The membrane suspensions were incubated on ice for 30 minutes and then centrifuged at 142 000 x g for 30 minutes.

10 Extraction of cytoskeletal and cytoskeletal-associated proteins.

- To extract cytoskeletal proteins, crude membrane vesicles from the P3 fraction membrane were suspended in a volume of Triton X-100 extraction buffer to give a protein: detergent ratio of 5:1. The composition of the Triton X-100 extraction buffer was based on the methods of Arai et al., *J. Neuroscience* 38: 348-357 (1994) and contained 2% Triton
- 15 X-100, 10mM Tris-HCl, 2mM MgCl₂, 1mM leupeptin, soybean trypsin inhibitor, PMSF and benzamidine. Membrane pellets were suspended by hand with a round-bottom teflon pestle, and placed on ice for 40 minutes. Insoluble cytoskeletal matrices were precipitated for 35 minutes at 142 000 x g in a Beckman TLA 120.2 rotor. The supernatant was defined as non-cytoskeletal-associated membrane or membrane--associated protein and was removed.
- 20 The remaining pellet was extracted with Triton X-100 a second time using the same conditions. We defined the final pellet as cytoskeletal and cytoskeletal-associated protein.

Solubilization of protein and analysis by SDS-PAGE and Western Blotting

- Membrane and cytoskeletal protein was solubilized in a minimum volume of 1% SDS, 3M urea, 0.1mM dithiothreitol in TBS buffer and sonicated. Protein concentration was
- 25 determined using the BioRad DC Protein assay and samples were diluted at least 1 X with 5 X sample buffer (250mM Tris-HCl pH 6.8, 10% SDS, 25% glycerol, 0.02% bromophenol blue and 7% 2-mercaptoethanol) and were loaded on 7.5% SDS-PAGE gels (Bio-Rad Mini-PROTEIN II Cell system) without boiling. Western blotting was performed as
- 30 described above.

Immunohistochemistry

Brain tissue was obtained from a normal C57BL/6 adult (6 months old) male mouse sacrificed with chloroform then perfusion-fixed with 4% v/v paraformaldehyde/0.01 M phosphate buffer (4% PFA). The brain tissues were removed, immersion fixed in 4% PFA for 1 day, washed in 0.01M phosphate buffered saline, pH 7.2 (PBS) for 2 days, and then equilibrated in 25% w/v sucrose PBS for 1 week. The samples were then snap-frozen in Tissue Tek molds by isopentane cooled in liquid nitrogen. After warming to -20 C, frozen blocks derived from frontal cortex, caudate/putamen, cerebellum and brainstem were cut into 14 mm sections for immunohistochemistry. Following washing in PBS, the tissue sections were blocked using 2.5% v/v normal goat serum for 1 hour at room temperature. Primary antibodies diluted with PBS were applied to sections overnight at 4 C. Optimal dilutions for the polyclonal antibodies BKP1 and HIP1 were 1:50. Using washes of 3 x 5 minutes in PBS at room temperature, sections were sequentially incubated with biotinylated secondary antibody and then an avidin-biotin complex reagent (Vecta Stain ABC Kit, Vector) for 60 minutes each at room temperature. Color was developed using 3-3'-diaminobenzidine tetrahydrochloride and ammonium nickel sulfate.

For controls, sections were treated as described above except that HIP1 antibody aliquots were preabsorbed with an excess of HIP1 peptide as well as a peptide unrelated to HIP1 prior to incubation with the tissue sections.

In situ hybridization

In situ hybridization was performed as previously described with some modification (Suzuki et al, *BBRC* 219: 708-713 (1996)). The RNA probes were prepared using the plasmid gt149 (Lin, B., et al., *Human Molec. Genet.* 2: 1541-1545 (1994)) or a 558 subclone of HIP1. The anti-sense and sense single-stranded RNA probes were synthesized using T3 and T7 RNA polymerases and the In Vitro Transcription Kit (Clontech) with the addition of [α^{35} S]-CTP (Amersham) to the reaction mixture. Sense RNA probes were used as negative controls. For HIP1 studies normal C57BL/6 mice were used. Huntingtin probes were tested on two different transgenic mouse strains expressing full-length huntingtin, cDNA HD10366 (44CAG) C57BL/6 mice and YAC HD10366(18CAG) FVB/N mice. Frozen brain sections

(10um thick) were placed onto silane-coated slides under RNase-free conditions. The hybridization solution contained 40% w/v formamide, 0.02M Tris-HCl (pH 8.0), 0.005M EDTA, 0.3 M NaCl, 0.01M sodium phosphate (pH 7.0), 1x Denhardt's solution, 10% w/v dextran sulfate (pH 7.0), 0.2% w/v sarcosyl, yeast tRNA (500mg/ml) and salmon sperm DNA (200mg/ml). The radiolabelled RNA probe was added to the hybridization solution to give 1 x 10⁶ cpm/200 ul/ section. Sections were covered with hybridization solution and incubated on formamide paper at 65 C for 18 hours. After hybridization, the slides were washed for 30 minutes sequentially with 2x SSC, 1x SSC and high stringency wash solution (50% formamide, 2x SSC and 0.1M dithiothreitol) at 65 C, followed by treatment with RNase A (1mg/ml) at 37 C for 30 minutes, then washed again and air-dried. The slides were first exposed on autoradiographic film (b-max, Amersham, UK) for 48 hours and developed for 4 minutes in Kodak D-19 followed by a 5 minute fixation in Fuji-fix. For longer exposures, the slides were dipped in autoradiographic emulsion (50% w/v in distilled water, NR-2, Konica, Japan), air-dried and exposed for 20 days at 4 C then developed as described. Sections were counterstained with methyl green or Giemsa solutions.

EXAMPLE 10

We determined a more precise location of the HIP1 gene on chromosome 7 in the context of a physical and genetic map of chromosome 7, and determined its genomic organization. HIP1 maps by FISH and RH mapping to chromosome band 7q11.23, which contains the chromosomal region commonly deleted in Williams-Beuren syndrome (WS). We used several methods to refine the mapping of HIP1 in this region. PCR screening of a chromosome 7-YAC-library (Scherer et al., *mammalian Genome* 3: 179-181 (1992)) with primers from the 3' UTR of HIP1 resulted in the identification of only a single positive YAC clone (HSC7E512). This YAC clone had previously been shown to map near the Williams syndrome commonly deleted region (Osborne et al., *Genomics* 45: 402-406 (1997)). The HIP1 cDNA was then used to screen a chromosome 7 specific cosmid library from the Lawrence Livermore National Laboratory (LL07NC01), and the RPCI genomic P1 derived artificial chromosome (PAC) library (Pieter de Jong, Rosswell Park, Buffalo, NY). Several PAC and cosmid clones that were already part of pre-assembled contigs in the Williams

syndrome region at 7q11.23 were identified (Fig 5). Restriction enzyme digestion, blot hybridization experiments and PCR screening confirmed that the clones contained the HIP1 gene.

We determined the exon-intron boundaries and intron sizes of HIP1. Primers were designed based on the sequence of the HIP1 transcript and used to sequence directly from the cosmid, PAC clone and long PCR products from PAC or genomic DNA. Whenever a PCR fragment generated was longer than predicted from the cDNA sequence, it was assumed to contain an intron. The size of the introns was determined by sequencing the intron directly or by PCR amplification of the introns from both genomic DNA and the cosmid or PAC clone from the region. Three sets of overlapping cosmids and a PAC clone that contain the entire coding sequence of HIP1 were characterized (Fig 5). Cosmid 181G10 and 250F2 were digested with EcoRI and cloned into the plasmid bluescript. Further sequences were generated from these plasmid subclones. Intron-exon boundary sequences were then identified by comparing HIP1 genomic and transcript sequence. The gene is contained within 75 kb and comprises 29 exons and 28 introns. The intron-exon boundary sequences are shown in Table 4, along with the exon and intron sizes. A graphic summary of these data is also shown in Fig. 5. Exons 1 to 28 contained the coding regions. The last and largest exon of the HIP1 gene was found to contain approximately 7 kb. Most of the intron-exon junctions followed the canonical GT-AG rule. An AT was found at the 3' splice site of exon 1 and an AC at the 5' splice site of exon 2. Sequence data from all the exon-intron borders of the coding region and 3'-UTR is set forth in Seq. ID Nos. 16-44. (These sequence have been deposited with GenBank as Accession Nos. AF052261 to AF052288).

Sequence analysis of previously published 5' untranslated region (GenBank accession U79734) revealed the possibility that the open reading frame extends upstream of the ATG in the exon 4 to a 5' ATG in exon 1. Although we failed to obtain any additional 5' sequences despite repeated 5' RACE analyses, an additional ATG, 284 bp upstream of the previously published exon 1 is in the same reading frame and has the surrounding sequence of TGCCATGTT which is similar to the AGCCATGGG, the consensus Kozak sequence (Kozak, M. *Nucl. Acids Res.* 15: 8125-8148 (1987)). If translated from this ATG, the protein would be highly homologous to the N-terminal portion of ZK370.3 and yeast Sla2 protein

(Fig. 6). The translated protein in the region of exons 1 to 3 shows an identity of >40% and similarity of >60% to the N-terminal part of ZK370.3. This suggests that the exons 1 to 3 are probably translated.

In western blot studies, HIP1 is identified as a 120 kd protein (11, 23), while the putative translation of the previously published cDNA gives a protein product of estimated molecular weight of approximately 100 kd. If HIP1 gene were translated from the ATG 284 bp upstream of the exon 1, the expected product would have an estimated molecular weight of 122 kd. RNA PCR studies with primers downstream of this ATG and primers in exon 7 amplify expected products of 576 and 600 bp. Taken together these data support the contention that exon 1 extends further 5' and that HIP1 gene is translated from the ATG in exon 1. Sequence analyses showed no TATA, CAAT box or any GC rich promoter sequence upstream of exon 1 ATG. The promoter prediction programs provided by the server <http://dot.imgen.bcm.tmc.edu:9331/seq.search/gene.search.html> did not predict any promoter upstream of the ATG at position -284, (position 0 corresponds to the first nucleotide of published cDNA, GenBank accession U79734). This suggests that HIP1 may have additional exons.

Finally, we evaluated HIP1 gene as a candidate gene for Huntington disease in families without CAG expansion. In a large study of 1022 patients with a clinical diagnosis of HD, no CAG repeat expansion was found in 12 patients who might represent phenocopies of HD. In at least three families, linkage studies have excluded the HD locus at 4p. Mutation in an interacting protein could result in a similar phenotype as illustrated by the discovery of mutations in dystrophin associated proteins in muscular dystrophies. A mutation in HIP1 may result in altered interaction of huntingtin and HIP1 and lead to cellular toxicity as a result of more HIP1 being free in the cytosol. Thus mutations in huntingtin interacting proteins genes may cause a phenotype suggestive of HD. We studied two of the larger families diagnosed with HD without CAG expansion in HD gene, with the highly informative marker D71816 which maps centromeric and very close to HIP1 gene. The clinical findings in both the families were compatible with a diagnosis of HD, although there were atypical features. In family 1733, HIP1 locus appears to be excluded, as there are two recombinants with the marker. Individuals II-5 and II-7 who do not share the haplotype with

the affected individuals are now 41 and 39 years old and have normal neurological examinations.

In the family 1602, a lod score of 1.92 is obtained with the marker D7S1816 at $\theta_{\max}=0$. Sequencing of all the coding exons did not reveal any mutation in any exon sequence. The promoter sequence has not been examined. Subsequently a whole genome scan revealed a higher lod scores for markers on chromosome 20p.

EXAMPLE 11

A mouse brain lambda ZAPII cDNA library (Stratagene # 93609) was screened with various mouse ESTs which showed homology to the human HIP1 cDNA sequence (see Fig. 7). The ESTs were initially isolated from the non-redundant Database of GenBank EST Division by performing a BLASTN using a fragment of the human HIP1 cDNA as the query. We obtained 4 different ESTs which showed homology to HIP1: 1) aa110840 (clone 520282) which is 399bp and shows 58% identity, at the nucleotide level, to position 1880 to 2259 of the HIP1 cDNA. 2) w82687 (clone 404331) which is 420bp and shows 66% identity, at the nucleotide level, to position 2750 to 2915 of the HIP1 cDNA. 3) aa138903 (clone 586510) which is 509bp and shows 88% identity, at the nucleotide level, to position 2763 to 2832 of the HIP1 cDNA. 4) aa388714 (569088) which is 404bp and shows 88% identity, at the nucleotide level, to position 2475 to 2692 of the HIP1 cDNA.

mHIP1:

Fifty nanograms of a 362bp KpnI & PvuII fragment of clone 569088 (containing EST aa388714) was radioactively labeled with $[32\text{-P}]\text{-dCTP}$ using random-priming. The probe was allowed to hybridize to filters containing $> 2 \times 10^5$ pfu/ml of the mouse brain lambda ZAPII cDNA library (Stratagene # 93609) overnight at 65°C in Church buffer (0.5M sodium phosphate buffer (pH 7.2), 2.7% SDS, 1mM EDTA). The filters were washed at room temperature for 15 minutes with 2XSSPE, 0.1% SDS, then at 65°C for 20 minutes with 1XSSPE, 0.1%SDS and finally twice at 65°C with 0.5 XSSPE, 0.1%SDS. The filters were exposed to X-ray film (Kodak, XAR5) overnight at -70°C . Primary positives were isolated, replated and subsequent secondary positives were hybridized and washed as for the primary

screen. The resulting positive phage was converted into plasmid DNA by conventional methods (Stratagene) and the cDNA termed 4n-n1, was isolated and sequenced 551bp and 541bp from the T7 and T3 end, respectively. 4n-n1 is 2.2kb in length and the T7 end showed 72% identity, at the nucleotide level, to position 1486 to 1715 of the HIP1 cDNA. The 2.2kb insert from 4n-n1 was excised using EcoR1. Fifty nanograms of the 2.2kb insert was used to produced a radioactive probe and used to screen the mouse brain lambda ZAPII cDNA library (Stratagene # 93609) in the same manner as above. The resulting positive phage was converted into plasmid DNA by conventional methods (Stratagene) and the cDNA termed mHIP1a, was isolated and completely sequenced. mHIP1 is 2.3kb in length and showed 85% identity, at the nucleotide level, to position 726 to 3072 of the HIP1 cDNA.

mHIP1a:

Fifty nanograms of a 1.3kb EcoRI & NcoI fragment of clone 404331 (containing EST w82687) was radioactively labeled with [32-P]-dCTP using random--priming. The probe was allowed to hybridize to filters containing $> 2 \times 10^5$ pfu/ml of the mouse brain lambda ZAPII cDNA library (Stratagene # 93609) overnight at 65°C in Church buffer (see above). The filters were washed at room temperature for 15 minutes with 2XSSPE, 0.1% SDS, then at 65°C for 20 minutes with 1XSSPE, 0.1%SDS and finally twice at 65°C with 0.2XSSPE, 0.1%SDS. The filters were exposed to X-ray film (Kodak, XAR5) overnight at -70°C.

Primary positives were isolated, replated and subsequent secondary positives were hybridized and washed as for the primary screen. The resulting positive phage was converted into plasmid DNA by conventional methods (Stratagene) and the cDNA termed mHIP1a, was isolated and completely sequenced. mHIP1a is 3.96 kb in length and shows 60% identity, at the nucleotide level, to position 12 to 2703 of the HIP1 cDNA.

EXAMPLE 12

HIP1a:

The entire mHIP1a cDNA sequence was used to screen the non-redundant Database of GenBank EST Division. We identified a human EST, T08283, which showed homology to

mHIP1a. T08383 (clone HIBBB80) is 391bp and shows 87% identity, at the nucleotide level, to position 2904 to 3113 of the mHIP1a cDNA.

Fifty nanograms of a 1.6kb HindIII & NotII fragment of clone 404331 (containing EST T08283) was radioactively labeled with [32-P]-dCTP using random-priming. The probe was allowed to hybridize to filters containing $> 2 \times 10^5$ pfu/ml of a human frontal cortex lambda cDNA library overnight at 65 C in Church buffer (see above). The filters were washed at 65 C for 10 minutes with 1XSSPE, 0.1% SDS, and then for 30 minutes and 15 minutes with 0.1XSSPE, 0.1%SDS. The filters were exposed to X-ray film (Kodak, XAR5) overnight at -70 C. Primary positives were isolated, replated and subsequent secondary positives were hybridized and washed as for the primary screen. The resulting positive phage was converted into plasmid DNA by conventional methods (Stratagene) and the cDNA termed HIP1a, was isolated and completely sequenced. HIP1a is 3.2 kb in length and shows 53% identity, at the nucleotide level, to position 876 to 3058 of the HIP1 cDNA.

EXAMPLE 13

Following the identification of a 1.2 kb partial human HIP-1 cDNA by yeast two-hybrid interaction studies, a 3.9 kb HIP-1 fragment was isolated from a cDNA library, ligated to a 5' RACE product then subcloned into the mammalian expression vector pCI-neo (Promega). This construct, CMV-HIP-1, expresses HIP-1 from the CMV promoter and was used in the cell expression studies described below. Mouse HIP-1a (mHIP-1a) was also subcloned into a CMV driven expression vector for cell culture expression studies.

EXAMPLE 14

Huntingtin proteins with expanded polyglutamine tracts can aggregate into large, irregularly shaped deposits in HD brains, transgenic mice and in vitro cell culture. We have shown that in HEK (human embryonic kidney) 293T cells the aggregation of full-length and larger huntingtin fragments occurs after the cells have been exposed to a period of apoptotic stress. In order to assess the consequence of HIP-1 expression in cultured cells, we used huntingtin aggregation as one marker of viability.

Human embryonic kidney cells (HEK 293T) were grown on glass coverslips in Dulbecco's modified Eagle medium (DMEM, Gibco, NY) with 10% fetal bovine serum and antibiotics, in 5% CO₂ at 37°C. The cells were transfected at 30% confluency with the calcium phosphate protocol by mixing Qiagen-prepared DNA (Qiagen, CA) with 2.5 M CaCl₂, then incubating at room temperature for 10 min. 2X HEPES buffer (240 mM NaCl, 3.0 mM Na₂HPO₄, 100 mM HEPES, pH 7.05) was added to the DNA/calcium mixture, incubated at 37°C for 60 sec, then added to the cells. After 12-18 h, the media was removed, the cells were washed and fresh media was added. At 36 h post-transfection, the cells were exposed to an apoptotic stress by treatment with 35 uM tamoxifen (Sigma) for 1 hour, or left untreated, then processed for immunofluorescence. The cells were washed with PBS, fixed in 4% paraformaldehyde/PBS solution for 20 minutes at room temperature then permeabilized in 0.5% Triton X-100/PBS for 5 min. Following three PBS washes, the cells were incubated with anti-huntingtin antibody MAB2166 (Chemicon) (1:2500 dilution) and anti-HIP-1 antibody HIP-1fp (1:100 dilution) in 0.4% BSA/PBS for 1 h at room temperature in a humidified container. The primary antibody was removed, the cells were washed and secondary antibodies conjugated to Texas red or FITC were added at a 1:600-1:800 dilution for 30 min at room temperature. The cells were then washed again, and the coverslips were mounted onto slides with DAPI (4',6'-diamindino-2 phenylindole, Sigma) as a nuclear counter-stain. Immunofluorescence was viewed using a Zeiss (Axioscope) microscope, digitally captured with a CCD camera (Princeton Instrument Inc.) and the images were colourized and overlapped using the Eclipse (Empix Imaging Inc.) software program. Appropriate control experiments were performed to determine the specificity of the antibodies, including secondary antibody only and mock transfected cells.

The huntingtin fragment HD1955 was used in the aggregation studies. This fragment represents the N-terminal 548 amino acids of huntingtin, and corresponds approximately to the polyglutamine-containing fragment produced by caspase 3 cleavage of huntingtin. Transfection of HD1955 with 15 polyglutamines (HD1955-15) results in a diffuse cytoplasmic distribution of the expressed protein. Transfection of HD1955 with 128 polyglutamines (HD1955-128) also results in diffuse cytoplasmic expression. However, exposure of cells transfected with HD1955-128 to tamoxifen results in a marked

redistribution of huntingtin. In 29% of cells expressing HD1955-128, the huntingtin protein appears as dense aggregates that are localized in the perinuclear area of the cell. In contrast, less than 1% of HD1955-128 expressing cells contain aggregates in the absence of tamoxifen, and 0% of HD1955-15 cells form aggregates in the presence or absence of tamoxifen treatment.

Co-transfection of HIP-1 and HD1955 was used to test the influence of HIP-1 on huntingtin aggregation. As a control, b-galactosidase was co-transfected with HD1955. In the control transfections, 1-2% of cells expressing HD1955-128 formed aggregates in the absence of tamoxifen, similar to HD1955-128 expressed alone. However, when HD1955-128 was co-expressed with HIP-1, an average of 14% of huntingtin-expressing cells contained aggregates with no tamoxifen treatment. Double-labeling demonstrated that the majority of the cells containing aggregates also expressed HIP-1, directly implicating HIP-1 in the increase in aggregation. Therefore, these results indicate that HIP-1 provides sufficient stress on the huntingtin-expressing cells to form aggregates, to the extent that tamoxifen is no longer necessary.

EXAMPLE 15

We next designed a series of experiments to identify a region of HIP-1 sufficient for inducing aggregate formation of HD1955-128. As described above, HIP-1 contains a domain with high homology to the death effector domains (DED) present in many apoptosis-related proteins. The DED domain of HIP-1 was ligated in-frame to HD1955-128, 3' from the caspase-3 cleavage site. Transfection of the resulting fusion protein with the DED ligated in the sense orientation (HD1955-128-DEDsense) resulted in a large number (30-50%) of cells containing aggregates, without tamoxifen incubation. In contrast, expression of a huntingtin-DED fusion protein with DED in the antisense orientation (HD1955-128-DEDantisense) did not have more aggregates than the HD1955-128 no tamoxifen control. Therefore, the DED domain of HIP-1 is sufficient to stress the cells, causing aggregate formation.

EXAMPLE 16

To directly assess the effect of HIP-1 expression on cell viability, mitochondrial function tests were performed on 293T cells transfected with HIP-1. The assessment of mitochondrial function, using the MTT assay (Carmichael et al., *Cancer Res.* 47: 936-942 (1987); Vistica et al., *Cancer Res.* 51: 2515-2520 (1991)), is a standard method to measure cell viability. The MTT assay quantitates the formation of a coloured substrate (formazan), with the mitochondria of viable cells forming more substrate than non-viable cells. Since decreased mitochondrial activity is an early consequence of many cellular toxins, the MTT assay provides an early indicator of cell damage.

For cell viability assays, HEK 293T cells were seeded at a density of 5×10^4 cells into 96-well plates and transfected with 0.1 ug or 0.08 ug HIP-1 or 0.1 ug of the control construct lacZ using the calcium phosphate method described above. At 24-36 hours post-transfection tamoxifen-treated cells were incubated for 2 hours in a 1:10 dilution of WST-1 reagent (Boehringer Mannheim) and release of formazan from mitochondria was quantified at 450 nm using an ELISA plate reader (Dynatech Laboratories) (Carmichael et al., 1987; Mosmann, *J. Immunol. Meth* 65: 55-63 (1983)). One way ANOVA and Newman-Keuls test were used for statistical analysis. The transfection efficiency, measured by β -galactosidase staining and immunofluoresence, was approximately 50%.

We have previously demonstrated that expression of mutant huntingtin results in increased susceptibility to an apoptotic stress induced by sub-lethal doses of tamoxifen in transfected 293T cells (Martindale et al., 1998). A similar assay was used to test the consequence of HIP-1 expression. With 0.1 ug transfected HIP-1 DNA, after 24 hr expression, HIP-1 resulted in increased cell death in response to tamoxifen, compared with the tamoxifen-treated β -galactosidase control ($p < 0.01$, $n=4$). Reducing the amount of transfected HIP-1 DNA to 0.08 ug also resulted in increased cell death compared with control ($p < 0.01$, $n=4$), indicating the high potency of HIP-1 (Fig. 8). Furthermore, increased cell death in cells transfected with HIP-1 was observed in the absence of apoptotic stress at 48 hrs post-transfection, but was so severe that it could not be accurately quantitated. Thus, an earlier time point (24 hr) had to be used for better reproducibility, using an apoptotic stress to unmask the phenotype.

In order to model a pathogenic interaction of HIP-1 and huntingtin in the HEK 293 mammalian cell system, HIP-1 was transfected into cell lines stably expressing huntingtin. Two cell lines were chosen for the initial studies, one line expressed the truncated HD1955 construct with 15 glutamines, and the second expressed the HD1955 with 128 repeats. Western blotting indicated that the cell lines expressed huntingtin at similar levels. To assess whether HIP-1 is toxic in the presence of mutant huntingtin, 0.1 ug HIP-1 DNA was transfected into the HD1955-128 cell line. Transfection of HIP-1 into the HD1955-15 cell line was used as the wild-type huntingtin control, and transfection of LacZ into both cell lines was the control for transfection-related toxicity (Figs 9A and 9B). MTT toxicity assays showed that HIP-1 in the presence of mutant huntingtin (HD1955-128) was significantly more toxic than HIP-1 with wild-type huntingtin (HD1955-15), $p < 0.001$, $n = 4$ (Fig. 9C). This toxicity was observed at 24 hr and 36 hr post-transfection. No tamoxifen was needed to unmask the phenotype, suggesting that the combined cell stress of HIP-1 with truncated huntingtin was sufficient to reduce cell viability over control.